

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/397,967DATE: 01/23/2001
TIME: 04:56:49

INPUT SET: S36307.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Ihle, James N.
Silvennoinen, Ollie
Witthuhn, Bruce A.

(ii) TITLE OF INVENTION: Jak Kinases and Regulation of Cytokine
Signal Transduction

(iii) NUMBER OF SEQUENCES: 16

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox
(B) STREET: 1100 New York Avenue, Suite 600
(C) CITY: Washington
(D) STATE: D.C.
(E) COUNTRY: U.S.A.
(F) ZIP: 20005-3934

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/397,967
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/665,574
(B) FILING DATE:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/097,997
(B) FILING DATE: 29-JUL-1993

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/118,968
(B) FILING DATE: 09-SEP-1993

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Bugaisky, Lawrence B.

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47 (B) REGISTRATION NUMBER: 35,086
48 (C) REFERENCE/DOCKET NUMBER: 0656.0370002/SLF/LBB
49
50 (ix) TELECOMMUNICATION INFORMATION:
51 (A) TELEPHONE: (202) 371-2600
52 (B) TELEFAX: (202) 371-2540
53
54
55 (2) INFORMATION FOR SEQ ID NO:1:
56
57 (i) SEQUENCE CHARACTERISTICS:
58 (A) LENGTH: 5 amino acids
59 (B) TYPE: amino acid
60 (D) TOPOLOGY: linear
61
62
63 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
64
65 Trp Ser Xaa Trp Ser
66 1 5
67
68 (2) INFORMATION FOR SEQ ID NO:2:
69
70 (i) SEQUENCE CHARACTERISTICS:
71 (A) LENGTH: 15 amino acids
72 (B) TYPE: amino acid
73 (D) TOPOLOGY: linear
74
75
76 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
77
78 Val Leu Pro Gln Asp Lys Glu Tyr Tyr Lys Val Lys Glu Pro Gly
79 1 5 10 15
80
81
82 (2) INFORMATION FOR SEQ ID NO:3:
83
84 (i) SEQUENCE CHARACTERISTICS:
85 (A) LENGTH: 15 amino acids
86 (B) TYPE: amino acid
87 (D) TOPOLOGY: linear
88
89
90
91 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
92
93 Ala Ile Glu Thr Asp Lys Glu Tyr Tyr Thr Val Lys Asp Asp Arg
94 1 5 10 15
95
96 (2) INFORMATION FOR SEQ ID NO:4:
97
98 (i) SEQUENCE CHARACTERISTICS:
99 (A) LENGTH: 15 amino acids

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100 (B) TYPE: amino acid
101 (D) TOPOLOGY: linear
102
103
104
105 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
106
107 Ala Val Pro Glu Gly His Glu Tyr Tyr Arg Val Arg Glu Asp Gly
108 1 5 10 15
109
110 (2) INFORMATION FOR SEQ ID NO:5:
111
112 (i) SEQUENCE CHARACTERISTICS:
113 (A) LENGTH: 19 amino acids
114 (B) TYPE: amino acid
115 (D) TOPOLOGY: linear
116
117
118
119 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
120
121 Asp Ser Gln Arg Lys Leu Gln Phe Tyr Glu Asp Lys His Gln Leu Pro
122 1 5 10 15
123
124 Ala Pro Lys
125
126 (2) INFORMATION FOR SEQ ID NO:6:
127
128 (i) SEQUENCE CHARACTERISTICS:
129 (A) LENGTH: 19 amino acids
130 (B) TYPE: amino acid
131 (D) TOPOLOGY: linear
132
133
134
135 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
136
137 Thr Leu Ile Glu Lys Glu Arg Phe Tyr Glu Ser Arg Cys Arg Pro Val
138 1 5 10 15
139
140 Thr Pro Ser
141
142 (2) INFORMATION FOR SEQ ID NO:7:
143
144 (i) SEQUENCE CHARACTERISTICS:
145 (A) LENGTH: 19 amino acids
146 (B) TYPE: amino acid
147 (D) TOPOLOGY: linear
148
149
150
151 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
152

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153 Ser Pro Ser Glu Lys Glu His Phe Tyr Gln Arg Gln His Arg Leu Pro
154 1 5 10 15
155
156 Glu Pro Ser
157
158 (2) INFORMATION FOR SEQ ID NO:8:
159
160 (i) SEQUENCE CHARACTERISTICS:
161 (A) LENGTH: 3629 base pairs
162 (B) TYPE: nucleic acid
163 (C) STRANDEDNESS: single
164 (D) TOPOLOGY: linear
165
166
167 (ix) FEATURE:
168 (A) NAME/KEY: CDS
169 (B) LOCATION: 94..3480
170
171
172 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
173
174 CGGGGGAACA AGATGTGAAC TGTTTTCCCT CCCCAGAAGA AGAGGCCCTT TTTTCCCTC 60
175
176 CCGCGAAGGC CAATGTTCTG AAAAAAGCTC TAG ATG GGA ATG GCC TGC CTT ACA 114
177 Met Gly Met Ala Cys Leu Thr
178 1 5
179
180 ATG ACA GAA ATG GAG GCA ACC TCC ACA TCT CCT GTA CAT CAG AAT GGT 162
181 Met Thr Glu Met Glu Ala Thr Ser Thr Ser Pro Val His Gln Asn Gly
182 10 15 20
183
184 GAT ATT CCT GGA AGT GCT AAT TCT GTG AAG CAG ATA GAG CCA GTC CTT 210
185 Asp Ile Pro Gly Ser Ala Asn Ser Val Lys Gln Ile Glu Pro Val Leu
186 25 30 35
187
188 CAA GTG TAT CTG TAC CAT TCT CTT GGG CAA GCT GAA GGA GAG TAT CTG 258
189 Gln Val Tyr Leu Tyr His Ser Leu Gly Gln Ala Glu Gly Glu Tyr Leu
190 40 45 50 55
191
192 AAG TTT CCA AGT GGA GAG TAT GTT GCA GAA GAA ATT TGT GTG GCT GCT 306
193 Lys Phe Pro Ser Ser Gly Glu Tyr Val Ala Glu Glu Ile Cys Val Ala Ala
194 60 65 70
195
196 TCT AAA GCT TGT GGT ATT ACG CCT GTG TAT CAT AAT ATG TTT GCG TTA 354
197 Ser Lys Ala Cys Gly Ile Thr Pro Val Tyr His Asn Met Phe Ala Leu
198 75 80 85
199
200 ATG AGT GAA ACC GAA AGG ATC TGG TAC CCA CCC AAT CAT GTC TTC CAC 402
201 Met Ser Glu Thr Glu Arg Ile Trp Tyr Pro Pro Asn His Val Phe His
202 90 95 100
203
204 ATA GAC GAG TCA ACC AGG CAT GAC ATA CTC TAC AGG ATA AGG TTC TAC 450
205 Ile Asp Glu Ser Thr Arg His Asp Ile Leu Tyr Arg Ile Arg Phe Tyr

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206	105	110	115	
207				
208	TTC CCT CAT TGG TAC TGT AGT GGC AGC AGC AGA ACC TAC AGA TAC GGA			498
209	Phe Pro His Trp Tyr Cys Ser Gly Ser Ser Arg Thr Tyr Arg Tyr Gly			
210	120	125	130	135
211				
212	GTG TCC CGT GGG GCT GAA GCT CCT CTG CTT GAT GAC TTT GTC ATG TCT			546
213	Val Ser Arg Gly Ala Glu Ala Pro Leu Leu Asp Asp Phe Val Met Ser			
214		140	145	150
215				
216	TAC CTT TTT GCT CAG TGG CGG CAT GAT TTT GTT CAC GGA TGG ATA AAA			594
217	Tyr Leu Phe Ala Gln Trp Arg His Asp Phe Val His Gly Trp Ile Lys			
218		155	160	165
219				
220	GTA CCT GTG ACT CAT GAA ACT CAG GAA GAG TGT CTT GGG ATG GCG GTG			642
221	Val Pro Val Thr His Glu Thr Gln Glu Glu Cys Leu Gly Met Ala Val			
222		170	175	180
223				
224	TTA GAC ATG ATG AGA ATA GCT AAG GAG AAA GAC CAG ACT CCA CTG GCT			690
225	Leu Asp Met Met Arg Ile Ala Lys Glu Lys Asp Gln Thr Pro Leu Ala			
226		185	190	195
227				
228	GTC TAT AAC TCT GTC AGC TAC AAG ACA TTC TTA CCA AAG TGC GTT CGA			738
229	Val Tyr Asn Ser Val Ser Tyr Lys Thr Phe Leu Pro Lys Cys Val Arg			
230	200	205	210	215
231				
232	GCG AAG ATC CAA GAC TAT CAC ATT TTA ACC CGG AAG CGA ATC AGG TAC			786
233	Ala Lys Ile Gln Asp Tyr His Ile Leu Thr Arg Lys Arg Ile Arg Tyr			
234		220	225	230
235				
236	AGA TTT CGC AGA TTC ATT CAG CAA TTC AGT CAA TGT AAA GCC ACT GCC			834
237	Arg Phe Arg Arg Phe Ile Gln Gln Phe Ser Gln Cys Lys Ala Thr Ala			
238		235	240	245
239				
240	AGG AAC CTA AAA CTT AAG TAT CTT ATA AAC CTG GAA ACC CTG CAG TCT			882
241	Arg Asn Leu Lys Leu Lys Tyr Leu Ile Asn Leu Glu Thr Leu Gln Ser			
242		250	255	260
243				
244	GCC TTC TAC ACA GAA CAG TTT GAA GTA AAA GAA TCT GCA AGA GGT CCT			930
245	Ala Phe Tyr Thr Glu Gln Phe Glu Val Lys Glu Ser Ala Arg Gly Pro			
246		265	270	275
247				
248	TCA GGT GAG GAG ATT TTT GCA ACC ATT ATA ATA ACT GGA AAC GGT GGA			978
249	Ser Gly Glu Glu Ile Phe Ala Thr Ile Ile Ile Thr Gly Asn Gly Gly			
250	280	285	290	295
251				
252	ATT CAG TGG TCA AGA GGG AAA CAT AAG GAA AGT GAG ACA CTG ACA GAA			1026
253	Ile Gln Trp Ser Arg Gly Lys His Lys Glu Ser Glu Thr Leu Thr Glu			
254		300	305	310
255				
256	CAG GAC GTA CAG TTA TAT TGT GAT TTC CCT GAT ATT ATT GAT GTC AGT			1074
257	Gln Asp Val Gln Leu Tyr Cys Asp Phe Pro Asp Ile Ile Asp Val Ser			
258		315	320	325

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SEQUENCE VERIFICATION REPORT
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Line

Error

Original Text

PAGE: 1

SEQUENCE MISSING ITEM REPORT
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< < THERE ARE NO ITEMS MISSING > >

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SEQUENCE CORRECTION REPORT
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INPUT SET: S36307.raw

Line	Original Text	Corrected Text
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